2 OIPE

RAW SEQUENCE LISTING   DATE: 07/30/2001
PATENT APPLICATION: US/09/765,272   TIME: 12:02:09

Input Set : N:\Crf3\RULE60\09765272.txt
Output Set: N:\CRF3\07302001\I765272.raw

SEQUENCE LISTING

```
  1 (1) GENERAL INFORMATION:
  5       (i) APPLICANT: Choi et. al.
  9      (ii) TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
 13     (iii) NUMBER OF SEQUENCES: 452
 17      (iv) CORRESPONDENCE ADDRESS:
 19           (A) ADDRESSEE: Human Genome Sciences, Inc.   ENTERED
 21           (B) STREET: 9410 Key West Avenue
 23           (C) CITY: Rockville
 25           (D) STATE: Maryland
 27           (E) COUNTRY: USA
 29           (F) ZIP: 20850
 33       (v) COMPUTER READABLE FORM:
 35           (A) MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
 37           (B) COMPUTER: HP Vectra 486/33
 39           (C) OPERATING SYSTEM: MSDOS version 6.2
 41           (D) SOFTWARE: ASCII Text
 45      (vi) CURRENT APPLICATION DATA:
C--> 47           (A) APPLICATION NUMBER: US/09/765,272
C--> 49           (B) FILING DATE: 22-Jan-2001
 51           (C) CLASSIFICATION:
 55     (vii) PRIOR APPLICATION DATA:
 57           (A) APPLICATION NUMBER: 08/961,083
 59           (B) FILING DATE:
 63    (viii) ATTORNEY/AGENT INFORMATION:
 65           (A) NAME: Brookes, A. Anders
 67           (B) REGISTRATION NUMBER: 36,373
 69           (C) REFERENCE/DOCKET NUMBER: PB340P2
C--> 73      (ix) TELECOMMUNICATION INFORMATION:
 75           (A) TELEPHONE: (301) 309-8504
 77           (B) TELEFAX: (301) 309-8512
 85 (2) INFORMATION FOR SEQ ID NO: 1:
 87       (i) SEQUENCE CHARACTERISTICS:
 88           (A) LENGTH: 1999 base pairs
 89           (B) TYPE: nucleic acid
 90           (C) STRANDEDNESS: double
 91           (D) TOPOLOGY: linear
 95      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 97 TAAAATCTAC GACAATAAAA ATCAACTCAT TGCTGACTTG GGTTCTGAAC GCCGCGTCAA        60
 99 TGCCCAAGCT AATGATATTC CCACAGATTT GGTTAAGGCA ATCGTTTCTA TCGAAGACCA       120
101 TCGCTTCTTC GACCACAGGG GGATTGATAC CATCCGTATC CTGGGAGCTT TCTTGCGCAA       180
103 TCTGCAAAGC AATTCCCTCC AAGGTGGATC AACTCTCACC CAACAGTTGA TTAAGTTGAC       240
105 TTACTTTTCA ACTTCGACTT CCGACCAGAC TATTTCTCGT AAGGCTCAGG AAGCTTGGTT       300
107 AGCGATTCAG TTAGAACAAA AAGCAACCAA GCAAGAAATC TTGACCTACT ATATAAATAA       360
109 GGTCTACATG TCTAATGGGA ACTATGGAAT GCAGACAGCA GCTCAAAACT ACTATGGTAA       420
111 AGACCTCAAT AATTTAAGTT TACCTCAGTT AGCCTTGCTG GCTGGAATGC CTCAGGCACC       480
113 AAACCAATAT GACCCCTATT CACATCCAGA AGCAGCCCAA GACCGCCGAA ACTTGGTCTT       540
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Output Set: N:\CRF3\07302001\I765272.raw

```
115 ATCTGAAATG AAAAATCAAG GCTACATCTC TGCTGAACAG TATGAGAAAG CAGTCAATAC    600
117 ACCAATTACT GATGGACTAC AAAGTCTCAA ATCAGCAAGT AATTACCCTG CTTACATGGA    660
119 TAATTACCTC AAGGAAGTCA TCAATCAAGT TGAAGAAGAA ACAGGCTATA ACCTACTCAC    720
121 AACTGGGATG GATGTCTACA CAAATGTAGA CCAAGAAGCT CAAAAACATC TGTGGGATAT    780
123 TTACAATACA GACGAATACG TTGCCTATCC AGACGATGAA TTGCAAGTCG CTTCTACCAT    840
125 TGTTGATGTT TCTAACGGTA AAGTCATTGC CCAGCTAGGA GCACGCCATC AGTCAAGTAA    900
127 TGTTTCCTTC GGAATTAACC AAGCAGTAGA AACAAACCGC GACTGGGGAT CAACTATGAA    960
129 ACCGATCACA GACTATGCTC CTGCCTTGGA GTACGGTGTC TACGATTCAA CTGCTACTAT   1020
131 CGTTCACGAT GAGCCCTATA ACTACCCTGG GACAAATACT CCTGTTTATA ACTGGGATAG   1080
133 GGGCTACTTT GGCAACATCA CCTTGCAATA CGCCCTGCAA CAATCGCGAA ACGTCCCAGC   1140
135 CGTGGAAACT CTAAACAAGG TCGGACTCAA CCGCGCCAAG ACTTTCCTAA ATGGTCTAGG   1200
137 AATCGACTAC CCAAGTATTC ACTACTCAAA TGCCATTTCA AGTAACACAA CCGAATCAGA   1260
139 CAAAAAATAT GGAGCAAGTA GTGAAAGAT GGCTGCTGCT TACGCTGCCT TTGCAAATGG   1320
141 TGGAACTTAC TATAAACCAA TGTATATCCA TAAAGTCGTC TTTAGTGATG GGAGTGAAAA   1380
143 AGAGTTCTCT AATGTCGGAA CTCGTGCCAT GAAGGAAACG ACAGCCTATA TGATGACCGA   1440
145 CATGATGAAA ACAGTCTTGA CTTATGGAAC TGGACGAAAT GCCTATCTTG CTTGGCTCCC   1500
147 TCAGGCTGGT AAAACAGGAA CCTCTAACTA TACAGACGAG GAAATTGAAA ACCACATCAA   1560
149 GACCTCTCAA TTTGTAGCAC CTGATGAACT ATTTGCTGGC TATACGCGTA AATATTCAAT   1620
151 GGCTGTATGG ACAGGCTATT CTAACCGTCT GACACCACTT GTAGGCAATG GCCTTACGGT   1680
153 CGCTGCCAAA GTTTACCGCT CTATGATGAC CTACCTGTCT GAAGGAAGCA ATCCAGAAGA   1740
155 TTGGAATATA CCAGAGGGGC TCTACAGAAA TGGAGAATTC GTATTTAAAA ATGGTGCTCG   1800
157 TTCTACGTGG AACTCACCTG CTCCACAACA ACCCCCATCA ACTGAAAGTT CAAGCTCATC   1860
159 ATCAGATAGT TCAACTTCAC AGTCTAGCTC AACCACTCCA AGCACAAATA ATAGTACGAC   1920
161 TACCAATCCT AACAATAATA CGCAACAATC AAATACAACC CCTGATCAAC AAAATCAGAA   1980
163 TCCTCAACCA GCACAACCA                                                 1999
```

165 (2) INFORMATION FOR SEQ ID NO: 2:
167   (i) SEQUENCE CHARACTERISTICS:
168   (A) LENGTH: 666 amino acids
169   (B) TYPE: amino acid
170   (C) STRANDEDNESS: single
171   (D) TOPOLOGY: linear
173   (ii) MOLECULE TYPE: protein
178   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
180   Lys Ile Tyr Asp Asn Lys Asn Gln Leu Ile Ala Asp Leu Gly Ser Glu
181   1   5   10   15
183   Arg Arg Val Asn Ala Gln Ala Asn Asp Ile Pro Thr Asp Leu Val Lys
184   20   25   30
186   Ala Ile Val Ser Ile Glu Asp His Arg Phe Phe Asp His Arg Gly Ile
187   35   40   45
189   Asp Thr Ile Arg Ile Leu Gly Ala Phe Leu Arg Asn Leu Gln Ser Asn
190   50   55   60
192   Ser Leu Gln Gly Gly Ser Thr Leu Thr Gln Gln Leu Ile Lys Leu Thr
193   65   70   75   80
195   Tyr Phe Ser Thr Ser Thr Ser Asp Gln Thr Ile Ser Arg Lys Ala Gln
196   85   90   95
198   Glu Ala Trp Leu Ala Ile Gln Leu Glu Gln Lys Ala Thr Lys Gln Glu
199   100   105   110
201   Ile Leu Thr Tyr Tyr Ile Asn Lys Val Tyr Met Ser Asn Gly Asn Tyr
202   115   120   125

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204	Gly	Met	Gln	Thr	Ala	Ala	Gln	Asn	Tyr	Tyr	Gly	Lys	Asp	Leu	Asn	Asn
205		130					135				140				
207	Leu	Ser	Leu	Pro	Gln	Leu	Ala	Leu	Leu	Ala	Gly	Met	Pro	Gln	Ala	Pro
208	145				150				155				160
210	Asn	Gln	Tyr	Asp	Pro	Tyr	Ser	His	Pro	Glu	Ala	Ala	Gln	Asp	Arg	Arg
211				165				170				175
213	Asn	Leu	Val	Leu	Ser	Glu	Met	Lys	Asn	Gln	Gly	Tyr	Ile	Ser	Ala	Glu
214			180					185				190
216	Gln	Tyr	Glu	Lys	Ala	Val	Asn	Thr	Pro	Ile	Thr	Asp	Gly	Leu	Gln	Ser
217		195				200				205
219	Leu	Lys	Ser	Ala	Ser	Asn	Tyr	Pro	Ala	Tyr	Met	Asp	Asn	Tyr	Leu	Lys
220		210				215				220
222	Glu	Val	Ile	Asn	Gln	Val	Glu	Glu	Glu	Thr	Gly	Tyr	Asn	Leu	Leu	Thr
223	225				230				235				240
225	Thr	Gly	Met	Asp	Val	Tyr	Thr	Asn	Val	Asp	Gln	Glu	Ala	Gln	Lys	His
226				245				250				255
228	Leu	Trp	Asp	Ile	Tyr	Asn	Thr	Asp	Glu	Tyr	Val	Ala	Tyr	Pro	Asp	Asp
229				260				265				270
231	Glu	Leu	Gln	Val	Ala	Ser	Thr	Ile	Val	Asp	Val	Ser	Asn	Gly	Lys	Val
232			275				280				285
234	Ile	Ala	Gln	Leu	Gly	Ala	Arg	His	Gln	Ser	Ser	Asn	Val	Ser	Phe	Gly
235		290				295				300
237	Ile	Asn	Gln	Ala	Val	Glu	Thr	Asn	Arg	Asp	Trp	Gly	Ser	Thr	Met	Lys
238	305				310				315				320
240	Pro	Ile	Thr	Asp	Tyr	Ala	Pro	Ala	Leu	Glu	Tyr	Gly	Val	Tyr	Asp	Ser
241				325				330				335
243	Thr	Ala	Thr	Ile	Val	His	Asp	Glu	Pro	Tyr	Asn	Tyr	Pro	Gly	Thr	Asn
244				340				345				350
246	Thr	Pro	Val	Tyr	Asn	Trp	Asp	Arg	Gly	Tyr	Phe	Gly	Asn	Ile	Thr	Leu
247			355				360				365
249	Gln	Tyr	Ala	Leu	Gln	Gln	Ser	Arg	Asn	Val	Pro	Ala	Val	Glu	Thr	Leu
250		370				375				380
252	Asn	Lys	Val	Gly	Leu	Asn	Arg	Ala	Lys	Thr	Phe	Leu	Asn	Gly	Leu	Gly
253	385				390				395				400
255	Ile	Asp	Tyr	Pro	Ser	Ile	His	Tyr	Ser	Asn	Ala	Ile	Ser	Ser	Asn	Thr
256				405				410				415
258	Thr	Glu	Ser	Asp	Lys	Lys	Tyr	Gly	Ala	Ser	Ser	Glu	Lys	Met	Ala	Ala
259				420				425				430
261	Ala	Tyr	Ala	Ala	Phe	Ala	Asn	Gly	Gly	Thr	Tyr	Tyr	Lys	Pro	Met	Tyr
262			435				440				445
264	Ile	His	Lys	Val	Val	Phe	Ser	Asp	Gly	Ser	Glu	Lys	Glu	Phe	Ser	Asn
265			450				455				460
267	Val	Gly	Thr	Arg	Ala	Met	Lys	Glu	Thr	Thr	Ala	Tyr	Met	Met	Thr	Asp
268	465				470				475				480
270	Met	Met	Lys	Thr	Val	Leu	Thr	Tyr	Gly	Thr	Gly	Arg	Asn	Ala	Tyr	Leu
271				485				490				495
273	Ala	Trp	Leu	Pro	Gln	Ala	Gly	Lys	Thr	Gly	Thr	Ser	Asn	Tyr	Thr	Asp
274			500				505				510
276	Glu	Glu	Ile	Glu	Asn	His	Ile	Lys	Thr	Ser	Gln	Phe	Val	Ala	Pro	Asp

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Input Set : **N:\Crf3\RULE60\09765272.txt**
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```
277            515              520                525
279    Glu Leu Phe Ala Gly Tyr Thr Arg Lys Tyr Ser Met Ala Val Trp Thr
280          530              535              540
282    Gly Tyr Ser Asn Arg Leu Thr Pro Leu Val Gly Asn Gly Leu Thr Val
283    545              550              555              560
285    Ala Ala Lys Val Tyr Arg Ser Met Met Thr Tyr Leu Ser Glu Gly Ser
286              565              570              575
288    Asn Pro Glu Asp Trp Asn Ile Pro Glu Gly Leu Tyr Arg Asn Gly Glu
289          580              585              590
291    Phe Val Phe Lys Asn Gly Ala Arg Ser Thr Trp Asn Ser Pro Ala Pro
292          595              600              605
294    Gln Gln Pro Pro Ser Thr Glu Ser Ser Ser Ser Ser Ser Asp Ser Ser
295          610              615              620
297    Thr Ser Gln Ser Ser Ser Thr Thr Pro Ser Thr Asn Asn Ser Thr Thr
298    625              630              635              640
300    Thr Asn Pro Asn Asn Asn Thr Gln Gln Ser Asn Thr Thr Pro Asp Gln
301              645              650              655
303    Gln Asn Gln Asn Pro Gln Pro Ala Gln Pro
304              660              665
```

306 (2) INFORMATION FOR SEQ ID NO: 3:
308   (i) SEQUENCE CHARACTERISTICS:
309   (A) LENGTH: 1714 base pairs
310   (B) TYPE: nucleic acid
311   (C) STRANDEDNESS: double
312   (D) TOPOLOGY: linear
316   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```
318 AAATTACAAT ACGGACTATG AATTGACCTC TGGAGAAAAA TTACCTCTTC CTAAAGAGAT   60
320 TTCAGGTTAC ACTTATATTG GATATATCAA AGAGGGAAAA ACGACTTCTG AGTCTGAAGT  120
322 AAGTAATCAA AAGAGTTCAG TTGCCACTCC TACAAAACAA CAAAAGGTGG ATTATAATGT  180
324 TACACCGAAT TTTGTAGACC ATCCATCAAC AGTACAAGCT ATTCAGGAAC AAACACCTGT  240
326 TTCTTCAACT AAGCCGACAG AAGTTCAAGT AGTTGAAAAA CCTTTCTCTA CTGAATTAAT  300
328 CAATCCAAGA AAAGAAGAGA AACAATCTTC AGATTCTCAA GAACAATTAG CCGAACATAA  360
330 GAATCTAGAA ACGAAGAAAG AGGAGAAGAT TTCTCCAAAA GAAAAGACTG GGGTAAATAC  420
332 ATTAAATCCA CAGGATGAAG TTTTATCAGG TCAATTGAAC AAACCTGAAC TCTTATATCG  480
334 TGAGGAAACT ATGGAGACAA AAATAGATTT TCAAGAAGAA ATTCAAGAAA ATCCTGATTT  540
336 AGCTGAAGGA ACTGTAAGAG TAAAACAAGA AGGTAAATTA GGTAAGAAAG TTGAAATCGT  600
338 CAGAATATTC TCTGTAAACA AGGAAGAAGT TTCGCGAGAA ATTGTTTCAA CTTCAACGAC  660
340 TGCGCCTAGT CCAAGAATAG TCGAAAAAGG TACTAAAAAA ACTCAAGTTA TAAAGGAACA  720
342 ACCTGAGACT GGTGTAGAAC ATAAGGACGT ACAGTCTGGA GCTATTGTTG AACCCGCAAT  780
344 TCAGCCTGAG TTGCCCGAAG CTGTAGTAAG TGACAAAGGC GAACCAGAAG TTCAACCTAC  840
346 ATTACCCGAA GCAGTTGTGA CCGACAAAGG TGAGACTGAG GTTCAACCAG AGTCGCCAGA  900
348 TACTGTGGTA AGTGATAAAG GTGAACCAGA GCAGGTAGCA CCGCTTCCAG AATATAAGGG  960
350 TAATATTGAG CAAGTAAAAC CTGAAACTCC GGTTGAGAAG ACCAAAGAAC AAGGTCCAGA 1020
352 AAAAACTGAA GAAGTTCCAG TAAAACCAAC AGAAGAAACA CCAGTAAATC CAAATGAAGG 1080
354 TACTACAGAA GGAACCTCAA TTCAAGAAGC AGAAAATCCA GTTCAACCTG CAGAAGAATC 1140
356 AACAACGAAT TCAGAGAAAG TATCACCAGA TACATCTAGC AAAAATACTG GGAAGTGTC  1200
358 CAGTAATCCT AGTGATTCGA CAACCTCAGT TGGAGAATCA AATAAACCAG AACATAATGA 1260
360 CTCTAAAAAT GAAAATTCAG AAAAAACTGT AGAAGAAGTT CCAGTAAATC CAAATGAAGG 1320
362 CACAGTAGAA GGTACCTCAA ATCAAGAAAC AGAAAAACCA GTTCAACCTG CAGAAGAAAC 1380
```

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PATENT APPLICATION: US/09/765,272   TIME: 12:02:09

Input Set : **N:\Crf3\RULE60\09765272.txt**
Output Set: **N:\CRF3\07302001\I765272.raw**

```
364 ACAAACAAAC TCTGGGAAAA TAGCTAACGA AAATACTGGA GAAGTATCCA ATAAACCTAG    1440
366 TGATTCAAAA CCACCAGTTG AAGAATCAAA TCAACCAGAA AAAAACGGAA CTGCAACAAA    1500
368 ACCAGAAAAT TCAGGTAATA CAACATCAGA GAATGGACAA ACAGAACCAG AACCATCAAA    1560
370 CGGAAATTCA ACTGAGGATG TTTCAACCGA ATCAAACACA TCCAATTCAA ATGGAAACGA    1620
372 AGAAATTAAA CAAGAAAATG AACTAGACCC TGATAAAAAG GTAGAAGAAC CAGAGAAAAC    1680
374 ACTTGAATTA AGAAATGTTT CCGACCTAGA GTTA                               1714
```

376 (2) INFORMATION FOR SEQ ID NO: 4:
378   (i) SEQUENCE CHARACTERISTICS:
379   (A) LENGTH: 571 amino acids
380   (B) TYPE: amino acid
381   (C) STRANDEDNESS: single
382   (D) TOPOLOGY: linear
384   (ii) MOLECULE TYPE: protein
389   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

```
391 Asn Tyr Asn Thr Asp Tyr Glu Leu Thr Ser Gly Glu Lys Leu Pro Leu
392 1               5                   10                  15
394 Pro Lys Glu Ile Ser Gly Tyr Thr Tyr Ile Gly Tyr Ile Lys Glu Gly
395             20                  25                  30
397 Lys Thr Thr Ser Glu Ser Glu Val Ser Asn Gln Lys Ser Ser Val Ala
398             35                  40                  45
400 Thr Pro Thr Lys Gln Gln Lys Val Asp Tyr Asn Val Thr Pro Asn Phe
401         50                  55                  60
403 Val Asp His Pro Ser Thr Val Gln Ala Ile Gln Glu Gln Thr Pro Val
404 65                  70                  75                  80
406 Ser Ser Thr Lys Pro Thr Glu Val Gln Val Val Glu Lys Pro Phe Ser
407             85                  90                  95
409 Thr Glu Leu Ile Asn Pro Arg Lys Glu Glu Lys Gln Ser Ser Asp Ser
410             100                 105                 110
412 Gln Glu Gln Leu Ala Glu His Lys Asn Leu Glu Thr Lys Lys Glu Glu
413         115                 120                 125
415 Lys Ile Ser Pro Lys Glu Lys Thr Gly Val Asn Thr Leu Asn Pro Gln
416         130                 135                 140
418 Asp Glu Val Leu Ser Gly Gln Leu Asn Lys Pro Glu Leu Leu Tyr Arg
419 145                 150                 155                 160
421 Glu Glu Thr Met Glu Thr Lys Ile Asp Phe Gln Glu Glu Ile Gln Glu
422             165                 170                 175
424 Asn Pro Asp Leu Ala Glu Gly Thr Val Arg Val Lys Gln Glu Gly Lys
425             180                 185                 190
427 Leu Gly Lys Lys Val Glu Ile Val Arg Ile Phe Ser Val Asn Lys Glu
428             195                 200                 205
430 Glu Val Ser Arg Glu Ile Val Ser Thr Ser Thr Thr Ala Pro Ser Pro
431         210                 215                 220
433 Arg Ile Val Glu Lys Gly Thr Lys Lys Thr Gln Val Ile Lys Glu Gln
434 225                 230                 235                 240
436 Pro Glu Thr Gly Val Glu His Lys Asp Val Gln Ser Gly Ala Ile Val
437             245                 250                 255
439 Glu Pro Ala Ile Gln Pro Glu Leu Pro Glu Ala Val Val Ser Asp Lys
440             260                 265                 270
442 Gly Glu Pro Glu Val Gln Pro Thr Leu Pro Glu Ala Val Val Thr Asp
```

VERIFICATION SUMMARY   DATE: 07/30/2001
PATENT APPLICATION: US/09/765,272   TIME: 12:02:10

Input Set : **N:\Crf3\RULE60\09765272.txt**
Output Set: **N:\CRF3\07302001\I765272.raw**

L:47 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:49 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:73 M:220 C: Keyword misspelled or invalid format, [(ix) TELECOMMUNICATION INFORMATION:]
L:853 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:2649 M:111 C: (47) String data converted to upper case,
M:111 Repeated in SeqNo=41
L:2885 M:111 C: (47) String data converted to upper case,
M:111 Repeated in SeqNo=45
L:2927 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46
L:2984 M:111 C: (47) String data converted to upper case,
M:111 Repeated in SeqNo=47
L:3320 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:52
L:3641 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:56
L:3825 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58
L:3828 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58
L:4317 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66
L:4395 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66
L:4966 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:74
L:5102 M:111 C: (47) String data converted to upper case,
M:111 Repeated in SeqNo=75
L:5172 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76
L:5365 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:80
L:5398 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:80
L:5533 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:82
L:7004 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:106
L:7007 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:106
L:7019 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:106
L:7034 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:106
L:7075 M:111 C: (47) String data converted to upper case,
M:111 Repeated in SeqNo=107
L:7616 M:111 C: (47) String data converted to upper case,
L:7764 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:118
L:7944 M:111 C: (47) String data converted to upper case,
L:8040 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:120
L:10220 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:160
L:10343 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:162
L:10809 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:172
L:10812 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:172
L:10815 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:172
L:11039 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:176
L:11932 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:194
L:14181 M:111 C: (47) String data converted to upper case,
L:17498 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:452